

## SEQUENCE LISTING

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 BOEHM, MANFRED

<120> HKIS COMPOSITIONS AND METHODS OF USE

<130> 8642/117

<140>

<141>

<150> 09/378,517

<151> 1999-08-20

<150> 60/097,710

<151> 1998-08-21

<160> 15

<170> PatentIn version 3.2

<210> 1

<211> 1260

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1257)

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gag gcc ttc ggg cgg ctg tgg cag gta cag agc cgt ctg ggt agc ggc	96
Glu Ala Phe Gly Arg Leu Trp Gln Val Gln Ser Arg Leu Gly Ser Gly	
20 25 30	
tcc tcc gcc tcg gtg tat cgg gtt cgc tgc tgc ggc aac cct ggc tcg	144
Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys Gly Asn Pro Gly Ser	
35 40 45	
ccc ccc ggc gcc ctc aag cag ttc ttg ccg cca gga acc acc ggg gct	192
Pro Pro Gly Ala Leu Lys Gln Phe Leu Pro Pro Gly Thr Thr Gly Ala	
50 55 60	
gcg gcc tct gcc gcc gag tat ggt ttc cgc aaa gag agg gcg gcg ctg	240
Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys Glu Arg Ala Ala Leu	
65 70 75 80	
gaa cag ttg cag ggt cac aga aac atc gtg act ttg tat gga gtg ttt	288
Glu Gln Leu Gln Gly His Arg Asn Ile Val Thr Leu Tyr Gly Val Phe	
85 90 95	

aca atc cac ttt tct cca aat gtg cca tca cgc tgt ctg ttg ctt gaa	336
Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg Cys Leu Leu Leu Glu	
100 105 110	
ctc ctg gat gtc agt gtt tcg gaa ttg ctc tta tat tcc agt cac cag	384
Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu Tyr Ser Ser His Gln	
115 120 125	
ggg tgt tcc atg tgg atg ata cag cat tgc gcc cga gat gtt ttg gag	432
Gly Cys Ser Met Trp Met Ile Gln His Cys Ala Arg Asp Val Leu Glu	
130 135 140	
gcc ctt gct ttt ctt cat cat gag ggc tat gtc cat gcg gac ctc aaa	480
Ala Leu Ala Phe Leu His His Glu Gly Tyr Val His Ala Asp Leu Lys	
145 150 155 160	
cca cgt aac ata ttg tgg agt gca gag aat gaa tgt ttt aaa ctc att	528
Pro Arg Asn Ile Leu Trp Ser Ala Glu Asn Glu Cys Phe Lys Leu Ile	
165 170 175	
gac ttt gga ctt agc ttc aaa gaa ggc aat cag gat gta aag tat att	576
Asp Phe Gly Leu Ser Phe Lys Glu Gly Asn Gln Asp Val Lys Tyr Ile	
180 185 190	
cag aca gac ggg tat cgg gct cca gaa gca gaa ttg caa aat tgc ttg	624
Gln Thr Asp Gly Tyr Arg Ala Pro Glu Ala Glu Leu Gln Asn Cys Leu	
195 200 205	
gcc cag gct ggc ctg cag agt gat aca gaa tgt acc tca gct gtt gat	672
Ala Gln Ala Gly Leu Gln Ser Asp Thr Glu Cys Thr Ser Ala Val Asp	
210 215 220	
ctg tgg agc cta gga atc att tta ctg gaa atg ttc tca gga atg aaa	720
Leu Trp Ser Leu Gly Ile Ile Leu Leu Glu Met Phe Ser Gly Met Lys	
225 230 235 240	
ctg aaa cat aca gtc aga tct cag gaa tgg aag gca aac agt tct gct	768
Leu Lys His Thr Val Arg Ser Gln Glu Trp Lys Ala Asn Ser Ser Ala	
245 250 255	
att att gat cac ata ttt gcc agt aaa gca gtg gtg aat gcc gca att	816
Ile Ile Asp His Ile Phe Ala Ser Lys Ala Val Val Asn Ala Ala Ile	
260 265 270	
cca gcc tat cac cta aga gac ctt atc aaa agc atg ctt cat gat gat	864
Pro Ala Tyr His Leu Arg Asp Leu Ile Lys Ser Met Leu His Asp Asp	
275 280 285	
cca agc aga aga att cct gct gaa atg gca ttg tgc agc cca ttc ttt	912
Pro Ser Arg Arg Ile Pro Ala Glu Met Ala Leu Cys Ser Pro Phe Phe	
290 295 300	
agc att cct ttt gcc cct cat att gaa gat ctg gtc atg ctt ccc act	960
Ser Ile Pro Phe Ala Pro His Ile Glu Asp Leu Val Met Leu Pro Thr	
305 310 315 320	

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Pro	Val	Leu	Arg	Leu	Leu	Asn	Val	Leu	Asp	Asp	Asp	Tyr	Leu	Gly	Asn	
				325					330					335		
gaa	gag	gaa	tat	gaa	gat	gtt	gta	gaa	gat	gta	aaa	gag	gag	tgt	caa	1056
Glu	Glu	Glu	Tyr	Glu	Asp	Val	Val	Glu	Asp	Val	Lys	Glu	Glu	Cys	Gln	
			340					345					350			
aaa	tat	gga	cca	gtg	gta	tct	cta	ctt	gtt	cca	aag	gaa	aat	cct	ggc	1104
Lys	Tyr		Pro	Val	Val	Ser	Leu	Leu	Val	Pro	Lys	Glu	Asn	Pro	Gly	
		355					360					365				
aga	gga	caa	gtc	ttt	gtt	gag	tat	gca	aat	gct	ggg	gat	tcc	aaa	gct	1152
Arg	Gly	Gln	Val	Phe	Val	Glu	Tyr	Ala	Asn	Ala	Gly	Asp	Ser	Lys	Ala	
	370					375					380					
gcg	cag	aaa	tta	ctg	act	gga	agg	atg	ttt	gat	ggg	aag	ttt	gtt	gtg	1200
Ala	Gln	Lys	Leu	Leu	Thr	Gly	Arg	Met	Phe	Asp	Gly	Lys	Phe	Val	Val	
385					390					395					400	
gct	aca	ttc	tac	ccg	ctg	agt	gcc	tac	aag	agg	gga	tat	ctg	tat	caa	1248
Ala	Thr	Phe	Tyr	Pro	Leu	Ser	Ala	Tyr	Lys	Arg	Gly	Tyr	Leu	Tyr	Gln	
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Thr	Leu	Leu														

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&lt;211&gt; 419

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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			20				25						30			
Ser	Ser	Ala	Ser	Val	Tyr	Arg	Val	Arg	Cys	Cys	Gly	Asn	Pro	Gly	Ser	
		35				40						45				
Pro	Pro	Gly	Ala	Leu	Lys	Gln	Phe	Leu	Pro	Pro	Gly	Thr	Thr	Gly	Ala	
	50				55						60					
Ala	Ala	Ser	Ala	Ala	Glu	Tyr	Gly	Phe	Arg	Lys	Glu	Arg	Ala	Ala	Leu	
65					70					75					80	
Glu	Gln	Leu	Gln	Gly	His	Arg	Asn	Ile	Val	Thr	Leu	Tyr	Gly	Val	Phe	
			85					90						95		
Thr	Ile	His	Phe	Ser	Pro	Asn	Val	Pro	Ser	Arg	Cys	Leu	Leu	Leu	Glu	
			100					105						110		
Leu	Leu	Asp	Val	Ser	Val	Ser	Glu	Leu	Leu	Leu	Tyr	Ser	Ser	His	Gln	
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<210> 3  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: hKIS mutant  
 K54R

<220>  
 <221> CDS  
 <222> (1)..(1257)

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gag gcc ttc ggg cgg ctg tgg cag gta cag agc cgt ctg ggt agc ggc 96  
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 20 25 30

tcc tcc gcc tcg gtg tat cgg gtt cgc tgc tgc ggc aac cct ggc tcg 144  
 Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys Gly Asn Pro Gly Ser  
 35 40 45

ccc ccc ggc gcc ctc agg cag ttc ttg ccg cca gga acc acc ggg gct 192  
 Pro Pro Gly Ala Leu Arg Gln Phe Leu Pro Pro Gly Thr Thr Gly Ala  
 50 55 60

gcg gcc tct gcc gcc gag tat ggt ttc cgc aaa gag agg gcg gcg ctg 240  
 Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys Glu Arg Ala Ala Leu  
 65 70 75 80

gaa cag ttg cag ggt cac aga aac atc gtg act ttg tat gga gtg ttt 288  
 Glu Gln Leu Gln Gly His Arg Asn Ile Val Thr Leu Tyr Gly Val Phe  
 85 90 95

aca atc cac ttt tct cca aat gtg cca tca cgc tgt ctg ttg ctt gaa 336  
 Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg Cys Leu Leu Leu Glu  
 100 105 110

ctc ctg gat gtc agt gtt tcg gaa ttg ctc tta tat tcc agt cac cag 384  
 Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu Tyr Ser Ser His Gln  
 115 120 125

ggt tgt tcc atg tgg atg ata cag cat tgc gcc cga gat gtt ttg gag 432  
 Gly Cys Ser Met Trp Met Ile Gln His Cys Ala Arg Asp Val Leu Glu  
 130 135 140

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 Ala Leu Ala Phe Leu His His Glu Gly Tyr Val His Ala Asp Leu Lys  
 145 150 155 160

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gac ttt gga ctt agc ttc aaa gaa ggc aat cag gat gta aag tat att	576
Asp Phe Gly Leu Ser Phe Lys Glu Gly Asn Gln Asp Val Lys Tyr Ile	
180 185 190	
cag aca gac ggg tat cgg gct cca gaa gca gaa ttg caa aat tgc ttg	624
Gln Thr Asp Gly Tyr Arg Ala Pro Glu Ala Glu Leu Gln Asn Cys Leu	
195 200 205	
gcc cag gct ggc ctg cag agt gat aca gaa tgt acc tca gct gtt gat	672
Ala Gln Ala Gly Leu Gln Ser Asp Thr Glu Cys Thr Ser Ala Val Asp	
210 215 220	
ctg tgg agc cta gga atc att tta ctg gaa atg ttc tca gga atg aaa	720
Leu Trp Ser Leu Gly Ile Ile Leu Leu Glu Met Phe Ser Gly Met Lys	
225 230 235 240	
ctg aaa cat aca gtc aga tct cag gaa tgg aag gca aac agt tct gct	768
Leu Lys His Thr Val Arg Ser Gln Glu Trp Lys Ala Asn Ser Ser Ala	
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Ile Ile Asp His Ile Phe Ala Ser Lys Ala Val Val Asn Ala Ala Ile	
260 265 270	
cca gcc tat cac cta aga gac ctt atc aaa agc atg ctt cat gat gat	864
Pro Ala Tyr His Leu Arg Asp Leu Ile Lys Ser Met Leu His Asp Asp	
275 280 285	
cca agc aga aga att cct gct gaa atg gca ttg tgc agc cca ttc ttt	912
Pro Ser Arg Arg Ile Pro Ala Glu Met Ala Leu Cys Ser Pro Phe Phe	
290 295 300	
agc att cct ttt gcc cct cat att gaa gat ctg gtc atg ctt ccc act	960
Ser Ile Pro Phe Ala Pro His Ile Glu Asp Leu Val Met Leu Pro Thr	
305 310 315 320	
cca gtg cta aga ctg ctg aat gtg ctg gat gat gat tat ctt ggg aat	1008
Pro Val Leu Arg Leu Leu Asn Val Leu Asp Asp Asp Tyr Leu Gly Asn	
325 330 335	
gaa gag gaa tat gaa gat gtt gta gaa gat gta aaa gag gag tgt caa	1056
Glu Glu Glu Tyr Glu Asp Val Val Glu Asp Val Lys Glu Glu Cys Gln	
340 345 350	
aaa tat gga cca gtg gta tct cta ctt gtt cca aag gaa aat cct ggc	1104
Lys Tyr Gly Pro Val Val Ser Leu Leu Val Pro Lys Glu Asn Pro Gly	
355 360 365	
aga gga caa gtc ttt gtt gag tat gca aat gct ggt gat tcc aaa gct	1152
Arg Gly Gln Val Phe Val Glu Tyr Ala Asn Ala Gly Asp Ser Lys Ala	
370 375 380	
gcg cag aaa tta ctg act gga agg atg ttt gat ggg aag ttt gtt gtg	1200
Ala Gln Lys Leu Leu Thr Gly Arg Met Phe Asp Gly Lys Phe Val Val	
385 390 395 400	

gct aca ttc tac ccg ctg agt gcc tac aag agg gga tat ctg tat caa 1248  
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acc ttg ctt taa 1260  
 Thr Leu Leu

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 <211> 419  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: hKIS mutant  
           K54R

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                     20                    25                    30  
 Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys Gly Asn Pro Gly Ser  
                     35                    40                    45  
 Pro Pro Gly Ala Leu Arg Gln Phe Leu Pro Pro Gly Thr Thr Gly Ala  
                     50                    55                    60  
 Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys Glu Arg Ala Ala Leu  
   65                    70                    75                    80  
 Glu Gln Leu Gln Gly His Arg Asn Ile Val Thr Leu Tyr Gly Val Phe  
                     85                    90                    95  
 Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg Cys Leu Leu Leu Glu  
                     100                    105                    110  
 Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu Tyr Ser Ser His Gln  
                     115                    120                    125  
 Gly Cys Ser Met Trp Met Ile Gln His Cys Ala Arg Asp Val Leu Glu  
                     130                    135                    140  
 Ala Leu Ala Phe Leu His His Glu Gly Tyr Val His Ala Asp Leu Lys  
   145                    150                    155                    160  
 Pro Arg Asn Ile Leu Trp Ser Ala Glu Asn Glu Cys Phe Lys Leu Ile  
                     165                    170                    175  
 Asp Phe Gly Leu Ser Phe Lys Glu Gly Asn Gln Asp Val Lys Tyr Ile  
                     180                    185                    190  
 Gln Thr Asp Gly Tyr Arg Ala Pro Glu Ala Glu Leu Gln Asn Cys Leu  
                     195                    200                    205

Ala Gln Ala Gly Leu Gln Ser Asp Thr Glu Cys Thr Ser Ala Val Asp  
 210 215 220

Leu Trp Ser Leu Gly Ile Ile Leu Leu Glu Met Phe Ser Gly Met Lys  
 225 230 235 240

Leu Lys His Thr Val Arg Ser Gln Glu Trp Lys Ala Asn Ser Ser Ala  
 245 250 255

Ile Ile Asp His Ile Phe Ala Ser Lys Ala Val Val Asn Ala Ala Ile  
 260 265 270

Pro Ala Tyr His Leu Arg Asp Leu Ile Lys Ser Met Leu His Asp Asp  
 275 280 285

Pro Ser Arg Arg Ile Pro Ala Glu Met Ala Leu Cys Ser Pro Phe Phe  
 290 295 300

Ser Ile Pro Phe Ala Pro His Ile Glu Asp Leu Val Met Leu Pro Thr  
 305 310 315 320

Pro Val Leu Arg Leu Leu Asn Val Leu Asp Asp Asp Tyr Leu Gly Asn  
 325 330 335

Glu Glu Glu Tyr Glu Asp Val Val Glu Asp Val Lys Glu Glu Cys Gln  
 340 345 350

Lys Tyr Gly Pro Val Val Ser Leu Leu Val Pro Lys Glu Asn Pro Gly  
 355 360 365

Arg Gly Gln Val Phe Val Glu Tyr Ala Asn Ala Gly Asp Ser Lys Ala  
 370 375 380

Ala Gln Lys Leu Leu Thr Gly Arg Met Phe Asp Gly Lys Phe Val Val  
 385 390 395 400

Ala Thr Phe Tyr Pro Leu Ser Ala Tyr Lys Arg Gly Tyr Leu Tyr Gln  
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Thr Leu Leu

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<211> 597

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 27 Mutant S10A

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ttaacccggg	acttgagaa	gcactgcaga	gacatggaag	aggcgagcca	gcgcaagtgg	180
aatttcgatt	ttcagaatca	caaaccctta	gagggcaagt	acgagtggca	agaggtggag	240
aagggcagct	tgcccagatt	ctactacaga	cccccgcggc	cccccaaagg	tgctgcaag	300
gtgccggcgc	aggagagcca	ggatgtcagc	gggagccgcc	cggcggcgcc	tttaattggg	360
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tctactcaaa	acaaaagagc	caacagaaca	gaagaaaatg	tttcagacgg	ttccccaat	540
gccggttctg	tggagcagac	gcccaagaag	cctggcctca	gaagacgtca	aacgtaa	597

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&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: p27 Mutant S10A

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Phe	Gly	Pro	Val	Asp	His	Glu	Glu	Leu	Thr	Arg	Asp	Leu	Glu	Lys	His	35	40	45	
Cys	Arg	Asp	Met	Glu	Glu	Ala	Ser	Gln	Arg	Lys	Trp	Asn	Phe	Asp	Phe	50	55	60	
Gln	Asn	His	Lys	Pro	Leu	Glu	Gly	Lys	Tyr	Glu	Trp	Gln	Glu	Val	Glu	65	70	75	80
Lys	Gly	Ser	Leu	Pro	Glu	Phe	Tyr	Tyr	Arg	Pro	Pro	Arg	Pro	Pro	Lys	85	90	95	
Gly	Ala	Cys	Lys	Val	Pro	Ala	Gln	Glu	Ser	Gln	Asp	Val	Ser	Gly	Ser	100	105	110	
Arg	Pro	Ala	Ala	Pro	Leu	Ile	Gly	Ala	Pro	Ala	Asn	Ser	Glu	Asp	Thr	115	120	125	
His	Leu	Val	Asp	Pro	Lys	Thr	Asp	Pro	Ser	Asp	Ser	Gln	Thr	Gly	Leu	130	135	140	
Ala	Glu	Gln	Cys	Ala	Gly	Ile	Arg	Lys	Arg	Pro	Ala	Thr	Asp	Asp	Ser	145	150	155	160
Ser	Thr	Gln	Asn	Lys	Arg	Ala	Asn	Arg	Thr	Glu	Glu	Asn	Val	Ser	Asp	165	170	175	
Gly	Ser	Pro	Asn	Ala	Gly	Ser	Val	Glu	Gln	Thr	Pro	Lys	Lys	Pro	Gly	180	185	190	
Leu	Arg	Arg	Arg	Gln	Thr	195													

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&lt;211&gt; 27

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p27KIP1CR5P primer

<400> 7

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27

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p27KIP1CR3P primer

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30

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p27KIP1NH23P primer

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28

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: p27KIP1CIIH5P primer

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27

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p575P primer

<400> 11

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27

<210> 12  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: p573P primer

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<210> 13  
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<210> 14  
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 <212> DNA  
 <213> Artificial Sequence

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<210> 15  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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